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SEQUENCE LISTING

<110> Ford, John
Mulero, Julio

<120> METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
POLYPEPTIDES

<130> 28111/35908

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<150> PCT/US99/16180

<151> 1999-07-16

<150> 09/350,836

<151> 1999-07-09

<150> 09/273,447

<151> 1999-03-19

<150> 09/244,444

<151> 1999-02-04

<150> 09/122,449

<151> 1998-07-24

<150> 09/118,205

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<170> PatentIn Ver. 2.0

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agcacttata agctctatac acatagttac ctgggatttg gattgaaagc tgcaagacta 240

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aaaagtgata taataaagga accaaggaga aaattcagaa ggaaagaaaa aattgcctct 180
gcaggtgtgc gagcaggatt gcttctgcaa caaaagcctc caccagcca catcttgga 240
aaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta tcc 290
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Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu
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Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr
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ttg tat gga att atg ttt gat gca ggg agc act gga act cga att cat 434
Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His
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gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta gaa 482
Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu
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ggg gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta gat 530
Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp
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caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg gcc 578
Gln Pro Lys Gln Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala
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aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta 626
Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu
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Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly	
210 215 220	
tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat aca	962
Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr	
225 230 235	
cat agt tac ctg gga ttt gga ttg aaa gct gca aga cta gca acc ctg	1010
His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu	
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Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala	
260 265 270	
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Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys	
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Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu	
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Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile	
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aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc tta	1442
Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu	
385 390 395	
cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg ggg	1490
Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly	
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gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat tgaggccacg	1539
Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His	
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 Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
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 Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80
 Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
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 Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
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 Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
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 Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
 195 200 205
 Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
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 Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
 225 230 235 240
 Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly

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245								250					255			
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Gln	Tyr 290	Gly	Gly	Asn	Gln	Glu 295	Gly	Glu	Val	Gly	Phe 300	Glu	Pro	Cys	Tyr	
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Ala 385	Leu	Leu	Lys	Asp	Gly 390	Phe	Gly	Phe	Ala	Asp 395	Ser	Thr	Val	Leu	Gln 400	
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Val	Cys	Ser	Ala	Val	Ser	His	Arg	Asn	Gln	Gln	Thr	Trp	Phe	Glu	Gly	
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atc	ttc	ctg	tct	tcc	atg	tgc	ccc	atc	aat	gtc	agc	gcc	agc	acc	ttg	144
Ile	Phe	Leu	Ser	Ser	Met	Cys	Pro	Ile	Asn	Val	Ser	Ala	Ser	Thr	Leu	
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Tyr	Gly	Ile	Met	Phe	Asp	Ala	Gly	Ser	Thr	Gly	Thr	Arg	Ile	His	Val	
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Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys	
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gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc cta aag	384
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115 120 125	
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Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr	
290 295 300	

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 Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
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 Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
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tta	ccg	aga	tgg	ttg	gaa	gca	gag	tgg	atc	ttt	ggg	ggt	gtg	aaa	tac	864
Leu	Pro	Arg	Trp	Leu	Glu	Ala	Glu	Trp	Ile	Phe	Gly	Gly	Val	Lys	Tyr	
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cag	tat	ggt	ggc	aac	caa	gaa	ggg	gag	gtg	ggc	ttt	gag	ccc	tgc	tat	912
Gln	Tyr	Gly	Gly	Asn	Gln	Glu	Gly	Glu	Val	Gly	Phe	Glu	Pro	Cys	Tyr	
	290					295					300					
gcc	gaa	gtg	ctg	agg	gtg	gta	cga	gga	aaa	ctt	cac	cag	cca	gag	gag	960
Ala	Glu	Val	Leu	Arg	Val	Val	Arg	Gly	Lys	Leu	His	Gln	Pro	Glu	Glu	
305					310					315				320		
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Val	Gln	Arg	Gly	Ser	Phe	Tyr	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Arg	Ala	
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gtt	gac	aca	gac	atg	att	gat	tat	gaa	aag	ggg	ggt	att	tta	aaa	gtt	1056
Val	Asp	Thr	Asp	Met	Ile	Asp	Tyr	Glu	Lys	Gly	Gly	Ile	Leu	Lys	Val	
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gaa	gat	ttt	gaa	aga	aaa	gcc	agg	gaa	gtg	tgt	gat	aac	ttg	gaa	aac	1104
Glu	Asp	Phe	Glu	Arg	Lys	Ala	Arg	Glu	Val	Cys	Asp	Asn	Leu	Glu	Asn	
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Lys	Gly	Ser	Val	Ser	Ile	Met	Thr	Gly	Gln	Asp	Glu	Gly	Ile	Phe	Ala
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 Val Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp
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 Phe Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala
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 Ser Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg
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 Ile His Val Tyr Thr Phe Val Gln Lys Met Pro
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- 19 -

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<220>

<223> Description of Artificial Sequence: primer

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<211> 21

<212> DNA

- 20 -

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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<223> Description of Artificial Sequence: primer

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<212> DNA

<213> Artificial Sequence

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<212> DNA

<213> Homo sapiens

<400> 24

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<213> Homo sapiens

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Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35             40             45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50             55             60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65             70             75             80

Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
          85             90             95

Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
100             105             110

Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
115             120             125

Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
130             135             140

Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
145             150             155             160

Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
          165             170             175

Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
180             185             190

Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
195             200             205

Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
210             215             220

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Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
225 230 235 240

Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
245 250 255

Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
260 265 270

Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
275 280 285

Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
290 295 300

Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
305 310 315 320

Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
325 330 335

Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
340 345 350

Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
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Ala Ala Val Leu Arg
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<210> 26

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<212> DNA

<213> Homo sapiens

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gcgcggtgca tggaatgggc tatgtga atg aaa aaa ggt atc cgt tat gaa act 174
Met Lys Lys Gly Ile Arg Tyr Glu Thr
1 5

tcc aga aaa acg agc tac att ttt cag cag ccg cag cac ggt cct tgg 222
Ser Arg Lys Thr Ser Tyr Ile Phe Gln Gln Pro Gln His Gly Pro Trp
10 15 20 25

caa aca agg atg aga aaa ata tcc aac cac ggg agc ctg cgg gtg gcg 270
Gln Thr Arg Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala
30 35 40

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aag	gtg	gca	tac	ccc	ctg	ggg	ctg	tgt	gtg	ggc	gtg	ttc	atc	tat	gtt	318
Lys	Val	Ala	Tyr	Pro	Leu	Gly	Leu	Cys	Val	Gly	Val	Phe	Ile	Tyr	Val	
			45					50					55			
gcc	tac	atc	aag	tgg	cac	cgg	gcc	acc	gcc	acc	cag	gcc	ttc	ttc	agc	366
Ala	Tyr	Ile	Lys	Trp	His	Arg	Ala	Thr	Ala	Thr	Gln	Ala	Phe	Phe	Ser	
		60					65				70					
atc	acc	agg	gca	gcc	ccg	ggg	gcc	cgg	tgg	ggc	cag	cag	gcc	cac	agc	414
Ile	Thr	Arg	Ala	Ala	Pro	Gly	Ala	Arg	Trp	Gly	Gln	Gln	Ala	His	Ser	
	75					80					85					
ccc	ctg	ggg	aca	gct	gca	gac	ggg	cac	gag	gtc	ttc	tac	ggg	atc	atg	462
Pro	Leu	Gly	Thr	Ala	Ala	Asp	Gly	His	Glu	Val	Phe	Tyr	Gly	Ile	Met	
90					95					100					105	
ttt	gat	gca	gga	agc	act	ggc	acc	cga	gta	cac	gtc	ttc	cag	ttc	acc	510
Phe	Asp	Ala	Gly	Ser	Thr	Gly	Thr	Arg	Val	His	Val	Phe	Gln	Phe	Thr	
				110					115					120		
cgg	ccc	ccc	aga	gaa	act	ccc	acg	tta	acc	cac	gaa	acc	ttc	aaa	gca	558
Arg	Pro	Pro	Arg	Glu	Thr	Pro	Thr	Leu	Thr	His	Glu	Thr	Phe	Lys	Ala	
			125					130					135			
gtg	aag	cca	ggc	ctt	tct	gcc	tat	gct	gat	gat	gtt	gaa	aag	agc	gct	606
Val	Lys	Pro	Gly	Leu	Ser	Ala	Tyr	Ala	Asp	Asp	Val	Glu	Lys	Ser	Ala	
		140					145					150				
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Gln	Gly	Ile	Arg	Glu	Leu	Leu	Asp	Val	Ala	Lys	Gln	Asp	Ile	Pro	Phe	
	155					160					165					
gac	ttc	tgg	aag	gcc	acc	cct	ctg	gtc	ctc	aag	gcc	aca	gct	ggc	tta	702
Asp	Phe	Trp	Lys	Ala	Thr	Pro	Leu	Val	Leu	Lys	Ala	Thr	Ala	Gly	Leu	
170					175					180					185	
cgc	ctg	tta	cct	gga	gaa	aag	gcc	cag	aag	tta	ctg	cag	aag	gtg	aaa	750
Arg	Leu	Leu	Pro	Gly	Glu	Lys	Ala	Gln	Lys	Leu	Leu	Gln	Lys	Val	Lys	
			190						195					200		
gaa	gta	ttt	aaa	gca	tcg	cct	ttc	ctt	gta	ggg	gat	gac	tgt	gtt	tcc	798
Glu	Val	Phe	Lys	Ala	Ser	Pro	Phe	Leu	Val	Gly	Asp	Asp	Cys	Val	Ser	
			205					210					215			
atc	atg	aac	gga	aca	gat	gaa	ggc	gtt	tcg	gcg	tgg	atc	acc	atc	aac	846
Ile	Met	Asn	Gly	Thr	Asp	Glu	Gly	Val	Ser	Ala	Trp	Ile	Thr	Ile	Asn	
		220					225					230				
ttc	ctg	aca	ggc	agc	ttg	aaa	act	cca	gga	ggg	agc	agc	gtg	ggc	atg	894
Phe	Leu	Thr	Gly	Ser	Leu	Lys	Thr	Pro	Gly	Gly	Ser	Ser	Val	Gly	Met	
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ctg	gac	ttg	ggc	gga	gga	tcc	act	cag	atc	gcc	ttc	ctg	cca	cgc	gtg	942
Leu	Asp	Leu	Gly	Gly	Gly	Ser	Thr	Gln	Ile	Ala	Phe	Leu	Pro	Arg	Val	
250					255					260					265	
gag	ggc	acc	ctg	cag	gcc	tcc	cca	ccc	ggc	tac	ctg	acg	gca	ctg	cgg	990
Glu	Gly	Thr	Leu	Gln	Ala	Ser	Pro	Pro	Gly	Tyr	Leu	Thr	Ala	Leu	Arg	
				270					275						280	

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Met Phe Asn Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu	
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Gly Leu Met Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln	
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Pro Ala Lys Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser	
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Phe Lys Gly Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly	
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Gln Lys Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser	
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Glu Val Leu Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val	
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<210> 27
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<212> PRT
<213> Homo sapiens
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Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro Leu Gly
  35          40          45
Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp His Arg
  50          55          60
Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala Pro Gly
  65          70          75
Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala Ala Asp
  85          90          95
Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly
  100         105         110
Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu Thr Pro
  115         120         125
Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu Ser Ala

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130	135	140
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Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly Glu Lys 180 185 190		
Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala Ser Pro 195 200 205		
Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr Asp Glu 210 215 220		
Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser Leu Lys 225 230 235 240		
Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly Gly Ser 245 250 255		
Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln Ala Ser 260 265 270		
Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr Tyr Lys 275 280 285		
Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala Arg Leu 290 295 300		
Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly Lys Glu 305 310 315 320		
Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp Glu His 325 330 335		
Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala Ser Leu 340 345 350		
His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn Arg Val 355 360 365		
His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe Ser Tyr 370 375 380		
Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu Lys Gly 385 390 395 400		
Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr Val Cys 405 410 415		
Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys Met Asp 420 425 430		
Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro Arg Ser 435 440 445		
Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr Ser Trp 450 455 460		

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Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg Gln Lys
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Ser Pro Ala Ser

<210> 28

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

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21

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oligonucleotide primer

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